

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2003, 14:23:30 ; Search time 86 Seconds
(without alignments)
3053.755 Million cell updates/sec

Title: US-10-021-698-111
Perfect score: 3258
Sequence: 1 MPACCSGSDVFQYETNKVTR.....RIRKEFPKSEQYSGFKSPY 595

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3235	99.3	1853	3	US-08-842-079-19 Sequence 19, Appl
2	3235	99.3	1853	4	US-09-638-857-19 Sequence 19, Appl
3	2677	82.2	3540	3	US-08-842-079-16 Sequence 16, Appl
4	2677	82.2	3540	4	US-09-638-857-16 Sequence 16, Appl
5	896	27.5	1750	4	US-09-016-434-831 Sequence 831, Appl
6	896	27.5	1762	2	US-08-742-621-2 Sequence 2, Appli
7	880.5	27.0	1206	3	US-09-191-608-21 Sequence 21, Appl
8	867	26.6	1997	2	US-08-750-134A-6 Sequence 6, Appli
9	867	26.6	1997	3	US-09-363-745-6 Sequence 6, Appli
10	773	23.7	2643	2	US-08-750-134A-10 Sequence 10, Appl
11	773	23.7	2643	3	US-09-363-745-10 Sequence 10, Appl
12	769.5	23.6	577	4	US-09-016-434-829 Sequence 829, App

13	740	22.7	1837	2	US-08-750-134A-4	Sequence 4, Appli
14	740	22.7	1837	3	US-09-363-745-4	Sequence 4, Appli
15	681.5	20.9	1243	3	US-09-191-136-15	Sequence 15, Appl
16	678.5	20.8	1753	2	US-08-750-134A-8	Sequence 8, Appli
17	678.5	20.8	1753	3	US-09-363-745-8	Sequence 8, Appli
18	669.5	20.5	1272	3	US-09-191-136-13	Sequence 13, Appl
19	656.5	20.2	1421	3	US-09-191-608-14	Sequence 14, Appl
20	656.5	20.2	1436	3	US-09-191-608-13	Sequence 13, Appl
21	633.5	19.4	1499	3	US-09-191-608-16	Sequence 16, Appl
22	627.5	19.3	1697	3	US-09-381-681-2	Sequence 2, Appli
23	624.5	19.2	1293	3	US-09-381-681-1	Sequence 1, Appli
24	624.5	19.2	1360	3	US-09-191-136-30	Sequence 30, Appl
25	607.5	18.6	1349	3	US-09-191-608-15	Sequence 15, Appl
26	438	13.4	248	4	US-09-016-434-195	Sequence 195, App
27	379.5	11.6	878	1	US-07-915-934-3	Sequence 3, Appli
28	379.5	11.6	878	1	US-08-325-743-3	Sequence 3, Appli
29	328.5	10.1	531	3	US-09-191-608-8	Sequence 8, Appli
30	128	3.9	910	3	US-09-191-608-2	Sequence 2, Appli
31	111	3.4	221	3	US-09-191-608-1	Sequence 1, Appli
32	109.5	3.4	396	3	US-09-191-136-28	Sequence 28, Appli
33	103.5	3.2	1704	4	US-09-252-991A-11910	Sequence 11910, A
c 34	103.5	3.2	1956	4	US-09-252-991A-12032	Sequence 12032, A
35	103.5	3.2	3390	4	US-09-252-991A-11981	Sequence 11981, A
36	100.5	3.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
37	100.5	3.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
38	99.5	3.1	2455	4	US-09-227-357-79	Sequence 79, Appl
39	99	3.0	1493	4	US-09-016-434-1175	Sequence 1175, Ap
40	98	3.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 41	97.5	3.0	1260	4	US-09-252-991A-10925	Sequence 10925, A
42	97.5	3.0	2348	3	US-09-393-554-10	Sequence 10, Appl
43	97	3.0	6168	4	US-09-071-035-457	Sequence 457, App
44	97	3.0	6168	4	US-09-071-035-461	Sequence 461, App
45	97	3.0	6168	4	US-09-071-035-465	Sequence 465, App

ALIGNMENTS

RESULT 1
US-08-842-079-19
; Sequence 19, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-08-842-079-19

Alignment Scores:	0	Length:	1853
Pred. No.:	3235.00	Matches:	591
Score:	99.33%	Conservative:	0
Best Local Similarity:	99.33%	Mismatches:	4
Query Match:	99.29%	Indels:	0
DB:	3	Gaps:	0

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Db 27 ATGCCGCGCTGCTGCAGCTGCAGTGATGTTTCCAGTATGAGACGACAAAGTCACTCGG 86

QY	21	IleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIlePheSerTyr	40
DB	87	ATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGTGATCATCTTTTCTTAC	146
QY	41	ValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProValIleSerSer	60
DB	147	GTTTGTCTTGGTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTTCATCAGTTCT	206
QY	61	ValHisThrLysValLysGlyIleAlaGluValLysGluGluIleValGluAsnGlyVal	80
DB	207	GTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAGAATGGAGTG	266
QY	81	LysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeuGlnGlyAsn	100
DB	267	AAGAAAGTTGGTGACAGTGCTTTTGACACCGCAGACTACACCTTCCCTTTCAGGGGAAC	326
QY	101	SerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluArgLeuCysPro	120
DB	327	TCCTTTCTTCGTGTGACAAACTTTCTCAAAACAGAAAGGCCAAGAGCAGCGGTGTGTGCC	386
QY	121	GluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLysGlyTyrMet	140
DB	387	GAGTATCCCAACCCCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAGGGATGGATG	446
QY	141	AspProGlnSerLysGlyIleGlnThrGlyArgCysValValHisGluGlyAsnGlnLys	160
DB	447	GACCCGCGAGAGCAAAAGGAATTCAGACCGGAAGGTGTGTAGTCATGAAGGAACCAAG	506
QY	161	ThrCysGluValSerAlaTrpCysProIleGluAlaValGluAlaProArgProAla	180
DB	507	ACCTGTGAAGTCTCTGCTGGTGGTCCCCCATCGAGGAGTGAAGAGGCCCCCGGCTGCT	566
QY	181	LeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAspPheProGly	200
DB	567	CTCTTGAACAGTGCCGAAAACCTTCACGTGCTCATCAAGAACATATATCGACTTCCCCGGC	626
QY	201	HisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThrPheHisLys	220
DB	627	CACAACTACACCCAGAGAAACATCTCTGCCAGGTTTAAACATCACCTTGATACCTCCACAAG	686
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DB	747	AATTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGCAATTGAGATCTACTGGGACTGC	806
QY	261	AsnLeuAspArgTrpPheHisCysArgProLysTyrSerPheArgArgLeuAspAsp	280
DB	807	AACCTAGACCGTTGGTTCCATCACTGCCATCCCAATACAGTTTCCGTCGCTTGCACGAC	866
QY	281	LysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLysTyrTyrLys	300
DB	867	AAGACCACCAACGTGTCTTGTACCTGGCTACAACCTTCAGATACGCCAAGTACTACAAG	926
QY	301	GluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPheAspIleLeu	320
DB	927	GAATAACAATGTTGAGAAACGGACTCTGATATAAAGTCTTCGGGATCCGTTTTCACATCCTG	986
QY	321	ValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIleGlySerThr	340
DB	987	GTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATCGGCTCAAC	1046
QY	341	LeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThrTyrSerSer	360
DB	1047	CTCTCCTACITTCGGTCTGGCCGCTGTGTTCATCGACTTCCCTCATCGACACTTACTCCAGT	1106
QY	361	AsnCysCysArgSerHisIleTyrProTrpCysLysCysGlnProCysValValAsn	380
DB	1107	AACTGTCTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCTAGCCCTGTGTGGTCAAC	1166
QY	381	GluTyrTyrTrpArgLysLysCysGluSerIleValGluProLysProThrLeuLysTyr	400

Db	1167	GAATACTACTACAGGAAGAGTGCAGTCCATTGTGGAGCCAAAGCCGACATTAAAGTAT	1226
Qy	401	ValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeuGlyArgSer	420
Db	1227	GTGTCCITTTGTGGATGAATCCACATTAGGATGGTGAACCAAGCAGCTACTAGGGAGAAAT	1286
Qy	421	LeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThrAspLeuSer	440
Db	1287	CTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACAGATTGTCC	1346
Qy	441	ArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGluGluIleGln	460
Db	1347	AGGCTGCCCTGGCCCTCCATGACACACCCCGATTCTCTGGACAACCAAGAGGAGATACAG	1406
Qy	461	LeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTirPcysGlnCysGly	480
Db	1407	CTGCTTAGAAAGAGCGGACTCCTAGATCCAGGGATAGCCCGTCTGGTGCACAGTGTGA	1466
Qy	481	ArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluGluLeuCysCysArg	500
Db	1467	AGTGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTGTGTGCGG	1526
Qy	501	LysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuValLeuSerArg	520
Db	1527	AAAAAGCCGGGGCTGCATCACCACCTCAGAGTGTTTCAAGAAAGCTGGTCTCTCCAGA	1586
Qy	521	HisValLeuGlnPheLeuLeuTyrGlnGluProLeuLeuAlaLeuAspValAspSer	540
Db	1587	CACGTCTCGAGTTCTCTCTGTCTTACCAGGAGCCCTGTGTGGCGTGGATGTGGATTCC	1646
Qy	541	ThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTirPcysGlySer	560
Db	1647	ACCAACAGCCGGCTCGGCACTGTGCCTACAGGTGTGTACGCCACCTGGCGCTTCGGCTCC	1706
Qy	561	GlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTirPcysGlyArgLysGlu	580
Db	1707	CAGGACATGGCTGACTTTTGCCATCTGTGCCCCAGCTGTGTGGCTGGAGGATCCGGAAAGAG	1766
Qy	581	PheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyr	595
Db	1767	TTTCCGAAGAGTGTAGGCGAGTACAGTGGCTTCAAGAGATCCTTAC	1811

RESULT 2

US-09-638-857-19
; Sequence 19, Application US/09638857
; Patent No. 6509163
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/09/638,857
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 08/842,079
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-638-857-19

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		Conservative:	
		Mismatches:	
		Indels:	

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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 08:42:43 ; Search time 224 Seconds
(without alignments)
10023.732 Million cell updates/sec

Title: US-10-021-698-19
Perfect score: 5087
Sequence: 1 gcttctgtggccctgtcag.....taaaaaaggatatataattt 5087

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1834.6	36.1	1853	4	US-09-638-857-19
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5	450	8.8	577	4	US-09-016-434-829
6	383.2	7.5	59065	4	US-09-813-817-3
7	383.2	7.5	59065	4	US-09-978-197-3
8	332	6.5	55298	4	US-09-491-356C-1
9	330.8	6.5	36651	4	US-09-738-894A-3
10	330.8	6.5	36651	4	US-09-964-469-3
11	328.4	6.5	15977	4	US-09-608-285A-59
12	326.8	6.4	14747	4	US-09-608-285A-42
13	326.8	6.4	14747	4	US-09-557-800C-42
14	323	6.3	36159	4	US-09-749-588-3
15	311.2	6.1	87350	3	US-08-781-891-79
16	311.2	6.1	87350	4	US-09-618-166-79
17	311.2	6.1	87543	4	US-09-791-211-3
18	309.8	6.1	45716	4	US-08-965-048-5
19	309.8	6.1	45989	4	US-08-965-048-6
20	307.6	6.0	14796	3	US-08-975-080-35
21	307.6	6.0	14796	3	US-09-630-706-10
22	307.6	6.0	14796	4	US-09-496-694B-3
23	307.2	6.0	162450	4	US-09-345-882-1
24	306	6.0	31571	1	US-08-323-443B-1
25	306	6.0	53526	3	US-08-658-136-2
26	306	6.0	53577	3	US-08-658-136-1
27	301.2	5.9	18853	4	US-09-820-005-3

c	28	298.8	5.9	50000	4	US-09-146-053-3	Sequence 3, Appli
	29	297.6	5.9	19650	4	US-09-819-989-3	Sequence 3, Appli
c	30	296.8	5.8	5262	4	US-08-520-373D-5	Sequence 5, Appli
	31	295.2	5.8	6235	3	US-09-305-384-5	Sequence 5, Appli
	32	295.2	5.8	6235	4	US-09-525-160B-6	Sequence 6, Appli
	33	295.2	5.8	6679	3	US-09-305-384-1	Sequence 1, Appli
	34	295.2	5.8	6679	4	US-09-525-160B-5	Sequence 5, Appli
c	35	293.8	5.8	6769	1	US-08-480-784-20	Sequence 20, Appl
c	36	293.8	5.8	6769	1	US-08-483-553-20	Sequence 20, Appl
c	37	293.8	5.8	6769	1	US-08-487-002-20	Sequence 20, Appl
c	38	293.8	5.8	6769	1	US-08-483-554B-20	Sequence 20, Appl
c	39	293.8	5.8	6769	1	US-08-488-011B-20	Sequence 20, Appl
c	40	293.8	5.8	6769	3	US-08-850-727-20	Sequence 20, Appl
c	41	293.8	5.8	6769	5	PCT-US95-10202-20	Sequence 20, Appl
c	42	293.8	5.8	6769	5	PCT-US95-10203-20	Sequence 20, Appl
c	43	293.8	5.8	6769	5	PCT-US95-10220-20	Sequence 20, Appl
c	44	293.2	5.8	7676	1	US-08-451-777A-7	Sequence 7, Appli
c	45	293.2	5.8	7676	2	US-08-451-778A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-842-079-19
; Sequence 19, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-08-842-079-19

Query Match	36.1%	Score	1834.6;	DB	3;	Length	1853;
Best Local Similarity	99.5%	Pred. No.	0;				
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						Gaps	0;
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Qy	108	TGAGACGAACAAAGTCACCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTT	167				
Db	65	TGAGACGAACAAAGTCACCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTT	124				
Qy	168	CCACGTGATCATCTTTTCTACGTTTGTCTTGTCTGCTGAGTGACAAGCTGTACCAGCG	227				
Db	125	CCACGTGATCATCTTTTCTACGTTTGTCTTGTCTGCTGAGTGACAAGCTGTACCAGCG	184				
Qy	228	GAAAGAGCCTGTCTATCATCTGTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAGA	287				
Db	185	GAAAGAGCCTGTCTATCATCTGTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAGA	244				
Qy	288	GGAGATCGTGGAGAAATGGAGTGAAGAAGTTGGTGACAGTGTCTTTGACACCGCAGACTA	347				
Db	245	GGAGATCGTGGAGAAATGGAGTGAAGAAGTTGGTGACAGTGTCTTTGACACCGCAGACTA	304				
Qy	348	CACCTTCCCTTTGCAGGGGAACCTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAAGG	407				
Db	305	CACCTTCCCTTTGCAGGGGAACCTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAAGG	364				

